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[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

General information about the entry

Entry name	**Q9Y272**
Primary accession number	**Q9Y272**
Secondary accession numbers	None
Entered in TrEMBL in	Release 12, November 1999
Sequence was last modified in	Release 12, November 1999
Annotations were last modified in	Release 23, February 2003

Name and origin of the protein

Protein name	**RAS-related protein**
Synonyms	**Activator of G-protein signaling** **RAS, dexamethasone-induced 1**
Gene name	**AGS1 or DEXRAS1 or RASD1**
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

References

[1] SEQUENCE FROM NUCLEIC ACID.
   TISSUE=Pituitary;
   Kemppainen R.J.";
   "Identification of human pituitary Dexras1.";
   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

[2] SEQUENCE FROM NUCLEIC ACID.
   TISSUE=Liver;
   Cismowski M.J., Takesono A., Ma C., Lizano J.S., Xie X., Fuernkranz H., Lanier S.M., Duzic E.;
   "Functional genomics in the yeast Saccharomyces cerevisiae: cloning of mammalian G-protein activators.";
   Nat. Biotechnol. 0:0-0(1999).

[3] SEQUENCE FROM NUCLEIC ACID.
   MEDLINE=20135605; PubMed=10673050; [NCBI, ExPASy, EBI, Israel, Japan]
   Tu Y., Wu C.;
   "Cloning, expression and characterization of a novel human Ras-related protein that is regulated by glucocorticoid hormone.";
   Biochim. Biophys. Acta 1489:452-456(1999).

[4] SEQUENCE FROM NUCLEIC ACID.
   Cismowski M.J., Xie X., Duzic E.;
   "Genomic sequence of the human ras-related G-protein activator AGS1.";
   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

[5] SEQUENCE FROM NUCLEIC ACID.
   TISSUE=Brain;
   Strausberg R.;
   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

[6] SEQUENCE FROM NUCLEIC ACID.
   TISSUE=Brain;
   Puhl H.L., Ikeda S.R., Aronstam R.S.;
   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL	AF153192; AAD34621.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF069506; AAD34206.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF172846; AAF01364.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF222979; AAG44256.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	BC018041; AAH18041.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF498923; AAM21071.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P10114; 1KAO. [HSSP ENTRY / PDB]
Ensembl	Q9Y272; Homo sapiens. [Entry / Contig view]
InterPro	IPR001806; Ras_trnsfrmng.
	IPR005225; Small_GTP.
	Graphical view of domain structure.
Pfam	PF00071; ras; 1.
PRINTS	PR00449; RASTRNSFRMNG.
TIGRFAMs	TIGR00231; small_GTP; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
ProtoMap	Q9Y272.
PRESAGE	Q9Y272.
ModBase	Q9Y272.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

GTP-binding.

Features

None

2/6/03 2:28 PM

Sequence information

Length: **281 AA**   Molecular weight: **31642 Da**   CRC64: **06C3C4417E4A69BD** [This is a checksum on the sequence]

```
          10          20          30          40          50          60
          |           |           |           |           |           |
MKLAAMIKKM CPSDSELSIP AKNCYRMVIL GSSKVGKTAI VSRFLTGRFE DAYTPTIEDF

          70          80          90         100         110         120
          |           |           |           |           |           |
HRKFYSIRGE VYQLDILDTS GNHPFPAMRR LSILTGDVFI LVFSLDNRDS FEEVQRLRQQ

         130         140         150         160         170         180
          |           |           |           |           |           |
ILDTKSCLKN KTKENVDVPL VICGNKGDRD FYREVDQREI EQLVGDDPQR CAYFEISAKK

         190         200         210         220         230         240
          |           |           |           |           |           |
NSSLDQMFRA LFAMAKLPSE MSPDLHRKVS VQYCDVLHKK ALRNKKLLRA GSGGGGGDPG

         250         260         270         280
          |           |           |           |
DAFGIVAPFA RRPSVHSDLM YIREKASAGS QAKDKERCVI S
```

Q9Y272 in FASTA format

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Direct BLAST submission at EMBnet-CH/SIB (Switzerland)

Direct BLAST submission at NCBI (Bethesda, USA)

ScanProsite, MotifScan

Tools
Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

Feature table viewer (Java)

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